D. Jiang

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/488,728

DATE: 05/16/2001
TIME: 16:07:03

Input Set : N:\Crf3\RULE60\09488728.txt
Output Set: N:\CRF3\05162001\I488728.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: Troutt, Anthony
(ii) TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
(iii) NUMBER OF SEQUENCES: 4
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98101
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple PowerMacintosh
(C) OPERATING SYSTEM: Apple Operating System 7.5.5
(D) SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
(vi) CURRENT APPLICATION DATA:
C--> **(A) APPLICATION NUMBER: US/09/488,728**
C--> **(B) FILING DATE: 20-Jan-2000**
(C) CLASSIFICATION:
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US/09/978,773
(B) FILING DATE: 26-NOV-1997
(A) APPLICATION NUMBER: USSN 60/052,525
(B) FILING DATE: 27 NOVEMBER 1996
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Perkins, Patricia Anne
(B) REGISTRATION NUMBER: 34,693
(C) REFERENCE/DOCKET NUMBER: 2623-A
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (206)587-0430
(B) TELEFAX: (206)
(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mouse
(vii) IMMEDIATE SOURCE:
(B) CLONE: IL-17 receptor
(ix) FEATURE:

ENTERED

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69          (A) NAME/KEY: CDS
70          (B) LOCATION: 121..2712
73     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
75 GTCGACTGGA ACGAGACGAC CTGCTGCCGA CGAGCGCCAG TCCTCGGCCG GGAAAGCCAT      60
77 CGCGGGCCCT CGCTGTCGCG CGGAGCCAGC TGCGAGCGCT CCGCGACCGG GCCGAGGGCT     120
79 ATG GCG ATT CGG CGC TGC TGG CCA CGG GTC GTC CCC GGG CCC GCG CTG       168
80 Met Ala Ile Arg Arg Cys Trp Pro Arg Val Val Pro Gly Pro Ala Leu
81   1               5                  10                  15
83 GGA TGG CTG CTT CTG CTG CTG AAC GTT CTG GCC CCG GGC CGC GCC TCC       216
84 Gly Trp Leu Leu Leu Leu Leu Asn Val Leu Ala Pro Gly Arg Ala Ser
85              20                  25                  30
87 CCG CGC CTC CTC GAC TTC CCG GCT CCG GTC TGC GCG CAG GAG GGG CTG       264
88 Pro Arg Leu Leu Asp Phe Pro Ala Pro Val Cys Ala Gln Glu Gly Leu
89          35                  40                  45
91 AGC TGC AGA GTC AAG AAT AGT ACT TGT CTG GAT GAC AGC TGG ATC CAC       312
92 Ser Cys Arg Val Lys Asn Ser Thr Cys Leu Asp Asp Ser Trp Ile His
93      50                  55                  60
95 CCC AAA AAC CTG ACC CCG TCT TCC CCA AAA AAC ATC TAT ATC AAT CTT       360
96 Pro Lys Asn Leu Thr Pro Ser Ser Pro Lys Asn Ile Tyr Ile Asn Leu
97  65                  70                  75                  80
99 AGT GTT TCC TCT ACC CAG CAC GGA GAA TTA GTC CCT GTG TTG CAT GTT       408
100 Ser Val Ser Ser Thr Gln His Gly Glu Leu Val Pro Val Leu His Val
101                 85                  90                  95
103 GAG TGG ACC CTG CAG ACA GAT GCC AGC ATC CTG TAC CTC GAG GGT GCA      456
104 Glu Trp Thr Leu Gln Thr Asp Ala Ser Ile Leu Tyr Leu Glu Gly Ala
105             100                 105                 110
107 GAG CTG TCC GTC CTG CAG CTG AAC ACC AAT GAG CGG CTG TGT GTC AAG      504
108 Glu Leu Ser Val Leu Gln Leu Asn Thr Asn Glu Arg Leu Cys Val Lys
109         115                 120                 125
111 TTC CAG TTT CTG TCC ATG CTG CAG CAT CAC CGT AAG CGG TGG CGG TTT      552
112 Phe Gln Phe Leu Ser Met Leu Gln His His Arg Lys Arg Trp Arg Phe
113     130                 135                 140
115 TCC TTC AGC CAC TTT GTG GTA GAT CCT GGC CAG GAG TAT GAA GTG ACT      600
116 Ser Phe Ser His Phe Val Val Asp Pro Gly Gln Glu Tyr Glu Val Thr
117 145                 150                 155                 160
119 GTT CAC CAC CTG CCG AAG CCC ATC CCT GAT GGG GAC CCA AAC CAC AAA      648
120 Val His His Leu Pro Lys Pro Ile Pro Asp Gly Asp Pro Asn His Lys
121                 165                 170                 175
123 TCC AAG ATC ATC TTT GTG CCT GAC TGT GAG GAC AGC AAG ATG AAG ATG      696
124 Ser Lys Ile Ile Phe Val Pro Asp Cys Glu Asp Ser Lys Met Lys Met
125             180                 185                 190
127 ACT ACC TCA TGC GTG AGC TCA GGC AGC CTT TGG GAT CCC AAC ATC ACT      744
128 Thr Thr Ser Cys Val Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr
129         195                 200                 205
131 GTG GAG ACC TTG GAC ACA CAG CAT CTG CGA GTG GAC TTC ACC CTG TGG      792
132 Val Glu Thr Leu Asp Thr Gln His Leu Arg Val Asp Phe Thr Leu Trp
133     210                 215                 220
135 AAT GAA TCC ACC CCC TAC CAG GTC CTG CTG GAA AGT TTC TCC GAC TCA      840
136 Asn Glu Ser Thr Pro Tyr Gln Val Leu Leu Glu Ser Phe Ser Asp Ser
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```
137 225                 230                 235                 240
139 GAG AAC CAC AGC TGC TTT GAT GTC GTT AAA CAA ATA TTT GCG CCC AGG      888
140 Glu Asn His Ser Cys Phe Asp Val Val Lys Gln Ile Phe Ala Pro Arg
141                 245                 250                 255
143 CAA GAA GAA TTC CAT CAG CGA GCT AAT GTC ACA TTC ACT CTA AGC AAG      936
144 Gln Glu Glu Phe His Gln Arg Ala Asn Val Thr Phe Thr Leu Ser Lys
145             260                 265                 270
147 TTT CAC TGG TGC TGC CAT CAC CAC GTG CAG GTC CAG CCC TTC TTC AGC      984
148 Phe His Trp Cys Cys His His His Val Gln Val Gln Pro Phe Phe Ser
149         275                 280                 285
151 AGC TGC CTA AAT GAC TGT TTG AGA CAC GCT GTG ACT GTG CCC TGC CCA     1032
152 Ser Cys Leu Asn Asp Cys Leu Arg His Ala Val Thr Val Pro Cys Pro
153     290                 295                 300
155 GTA ATC TCA AAT ACC ACA GTT CCC AAG CCA GTT GCA GAC TAC ATT CCC     1080
156 Val Ile Ser Asn Thr Thr Val Pro Lys Pro Val Ala Asp Tyr Ile Pro
157 305                 310                 315                 320
159 CTG TGG GTG TAT GGC CTC ATC ACA CTC ATC GCC ATT CTG CTG GTG GGA     1128
160 Leu Trp Val Tyr Gly Leu Ile Thr Leu Ile Ala Ile Leu Leu Val Gly
161                 325                 330                 335
163 TCT GTC ATC GTG CTG ATC ATC TGT ATG ACC TGG AGG CTT TCT GGC GCC     1176
164 Ser Val Ile Val Leu Ile Ile Cys Met Thr Trp Arg Leu Ser Gly Ala
165             340                 345                 350
167 GAT CAA GAG AAA CAT GGT GAT GAC TCC AAA ATC AAT GGC ATC TTG CCC     1224
168 Asp Gln Glu Lys His Gly Asp Asp Ser Lys Ile Asn Gly Ile Leu Pro
169         355                 360                 365
171 GTA GCA GAC CTG ACT CCC CCA CCC CTG AGG CCC AGG AAG GTC TGG ATC     1272
172 Val Ala Asp Leu Thr Pro Pro Pro Leu Arg Pro Arg Lys Val Trp Ile
173     370                 375                 380
175 GTC TAC TCG GCC GAC CAC CCC CTC TAT GTG GAG GTG GTC CTA AAG TTC     1320
176 Val Tyr Ser Ala Asp His Pro Leu Tyr Val Glu Val Val Leu Lys Phe
177 385                 390                 395                 400
179 GCC CAG TTC CTG ATC ACT GCC TGT GGC ACT GAA GTA GCC CTT GAC CTC     1368
180 Ala Gln Phe Leu Ile Thr Ala Cys Gly Thr Glu Val Ala Leu Asp Leu
181                 405                 410                 415
183 CTG GAA GAG CAG GTT ATC TCT GAG GTG GGG GTC ATG ACC TGG GTG AGC     1416
184 Leu Glu Glu Gln Val Ile Ser Glu Val Gly Val Met Thr Trp Val Ser
185             420                 425                 430
187 CGA CAG AAG CAG GAG ATG GTG GAG AGC AAC TCC AAA ATC ATC ATC CTG     1464
188 Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser Lys Ile Ile Ile Leu
189         435                 440                 445
191 TGT TCC CGA GGC ACC CAA GCA AAG TGG AAA GCT ATC TTG GGT TGG GCT     1512
192 Cys Ser Arg Gly Thr Gln Ala Lys Trp Lys Ala Ile Leu Gly Trp Ala
193     450                 455                 460
195 GAG CCT GCT GTC CAG CTA CGG TGT GAC CAC TGG AAG CCT GCT GGG GAC     1560
196 Glu Pro Ala Val Gln Leu Arg Cys Asp His Trp Lys Pro Ala Gly Asp
197 465                 470                 475                 480
199 CTT TTC ACT GCA GCC ATG AAC ATG ATC CTG CCA GAC TTC AAG AGG CCA     1608
200 Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro Asp Phe Lys Arg Pro
201                 485                 490                 495
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```
203 GCC TGC TTC GGC ACC TAC GTT GTT TGC TAC TTC AGT GGC ATC TGT AGT      1656
204 Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe Ser Gly Ile Cys Ser
205             500                 505                 510
207 GAG AGG GAT GTC CCC GAC CTC TTC AAC ATC ACC TCC AGG TAC CCA CTC      1704
208 Glu Arg Asp Val Pro Asp Leu Phe Asn Ile Thr Ser Arg Tyr Pro Leu
209         515                 520                 525
211 ATG GAC AGA TTT GAG GAG GTT TAC TTC CGG ATC CAG GAC CTG GAG ATG      1752
212 Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile Gln Asp Leu Glu Met
213     530                 535                 540
215 TTT GAA CCC GGC CGG ATG CAC CAT GTC AGA GAG CTC ACA GGG GAC AAT      1800
216 Phe Glu Pro Gly Arg Met His His Val Arg Glu Leu Thr Gly Asp Asn
217 545                 550                 555                 560
219 TAC CTG CAG AGC CCT AGT GGC CGG CAG CTC AAG GAG GCT GTG CTT AGG      1848
220 Tyr Leu Gln Ser Pro Ser Gly Arg Gln Leu Lys Glu Ala Val Leu Arg
221                 565                 570                 575
223 TTC CAG GAG TGG CAA ACC CAG TGC CCC GAC TGG TTC GAG CGT GAG AAC      1896
224 Phe Gln Glu Trp Gln Thr Gln Cys Pro Asp Trp Phe Glu Arg Glu Asn
225             580                 585                 590
227 CTC TGC TTA GCT GAT GGC CAA GAT CTT CCC TCC CTG GAT GAA GAA GTG      1944
228 Leu Cys Leu Ala Asp Gly Gln Asp Leu Pro Ser Leu Asp Glu Glu Val
229         595                 600                 605
231 TTT GAA GAC CCA CTG CTG CCA CCA GGG GGA GGA ATT GTC AAA CAG CAG      1992
232 Phe Glu Asp Pro Leu Leu Pro Pro Gly Gly Gly Ile Val Lys Gln Gln
233     610                 615                 620
235 CCC CTG GTG CGG GAA CTC CCA TCT GAC GGC TGC CTT GTG GTA GAT GTC      2040
236 Pro Leu Val Arg Glu Leu Pro Ser Asp Gly Cys Leu Val Val Asp Val
237 625                 630                 635                 640
239 TGT GTC AGT GAG GAA GAA AGT AGA ATG GCA AAG CTG GAC CCT CAG CTA      2088
240 Cys Val Ser Glu Glu Glu Ser Arg Met Ala Lys Leu Asp Pro Gln Leu
241                 645                 650                 655
243 TGG CCA CAG AGA GAG CTA GTG GCT CAC ACC CTC CAA AGC ATG GTG CTG      2136
244 Trp Pro Gln Arg Glu Leu Val Ala His Thr Leu Gln Ser Met Val Leu
245             660                 665                 670
247 CCA GCA GAG CAG GTC CCT GCA GCT CAT GTG GTG GAG CCT CTC CAT CTC      2184
248 Pro Ala Glu Gln Val Pro Ala Ala His Val Val Glu Pro Leu His Leu
249         675                 680                 685
251 CCA GAC GGC AGT GGA GCA GCT GCC CAG CTG CCC ATG ACA GAG GAC AGC      2232
252 Pro Asp Gly Ser Gly Ala Ala Ala Gln Leu Pro Met Thr Glu Asp Ser
253     690                 695                 700
255 GAG GCT TGC CCG CTG CTG GGG GTC CAG AGG AAC AGC ATC CTT TGC CTC      2280
256 Glu Ala Cys Pro Leu Leu Gly Val Gln Arg Asn Ser Ile Leu Cys Leu
257 705                 710                 715                 720
259 CCC GTG GAC TCA GAT GAC TTG CCA CTC TGT AGC ACC CCA ATG ATG TCA      2328
260 Pro Val Asp Ser Asp Asp Leu Pro Leu Cys Ser Thr Pro Met Met Ser
261                 725                 730                 735
263 CCT GAC CAC CTC CAA GGC GAT GCA AGA GAG CAG CTA GAA AGC CTA ATG      2376
264 Pro Asp His Leu Gln Gly Asp Ala Arg Glu Gln Leu Glu Ser Leu Met
265             740                 745                 750
267 CTC TCG GTG CTG CAG CAG AGC CTG AGT GGA CAG CCC CTG GAG AGC TGG      2424
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```
268 Leu Ser Val Leu Gln Gln Ser Leu Ser Gly Gln Pro Leu Glu Ser Trp
269         755                 760                 765
271 CCG AGG CCA GAG GTG GTC CTC GAG GGC TGC ACA CCC TCT GAG GAG GAG      2472
272 Pro Arg Pro Glu Val Val Leu Glu Gly Cys Thr Pro Ser Glu Glu Glu
273     770                 775                 780
275 CAG CGG CAG TCG GTG CAG TCG GAC CAG GGC TAC ATC TCC AGG AGC TCC      2520
276 Gln Arg Gln Ser Val Gln Ser Asp Gln Gly Tyr Ile Ser Arg Ser Ser
277 785                 790                 795                 800
279 CCG CAG CCC CCC GAG TGG CTC ACG GAG GAG GAA GAG CTA GAA CTG GGT      2568
280 Pro Gln Pro Pro Glu Trp Leu Thr Glu Glu Glu Glu Leu Glu Leu Gly
281                 805                 810                 815
283 GAG CCC GTT GAG TCT CTC TCT CCT GAG GAA CTA CGG AGC CTG AGG AAG      2616
284 Glu Pro Val Glu Ser Leu Ser Pro Glu Glu Leu Arg Ser Leu Arg Lys
285             820                 825                 830
287 CTC CAG AGG CAG CTT TTC TTC TGG GAG CTC GAG AAG AAC CCT GGC TGG      2664
288 Leu Gln Arg Gln Leu Phe Phe Trp Glu Leu Glu Lys Asn Pro Gly Trp
289         835                 840                 845
291 AAC AGC TTG GAG CCA CGG AGA CCC ACC CCA GAA GAG CAG AAT CCC TCC      2712
292 Asn Ser Leu Glu Pro Arg Arg Pro Thr Pro Glu Glu Gln Asn Pro Ser
293     850                 855                 860
295 TAG GCCTCCTGAG CCTGCTACTT AAGAGGGTGT ATATTGTACT CTGTGTGTGC           2765
297 GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT    2825
299 GTGTGTGTAG TGCCCGGCTT AGAAATGTGA ACATCTGAAT CTGACATAGT GTTGTATACC    2885
301 TGAAGTCCCA GCACTTGGGA ACTGAGACTT GATGATCTCC TGAAGCCAGG TGTTCAGGGC    2945
303 CAGTGTGAAA ACATAGCAAG ACCTCAGAGA AATCAATGCA GACATCTTGG TACTGATCCC    3005
305 TAAACACACC CCTTTCCCTG ATAACCCGAC ATGAGCATCT GGTCATCATT GCACAAGAAT    3065
307 CCACAGCCCG TTCCCAGAGC TCATAGCCAA GTGTGTTGCT CATTCCTTGA ATATTTATTC    3125
309 TGTACCTACT ATTCATCAGA CATTTGGAAT TCAAAAACAA GTTACATGAC ACAGCCTTAG    3185
311 CCACTAAGAA GCTTAAAATT CGGTAAGGAT GTAAAATTAG CCAGGATGAA TAGAGGGCTG    3245
313 CTGCCCTGGC TGCAGAAGAG CAGGTCGTCT CGTTCCAGTC GAC                      3288
316 (2) INFORMATION FOR SEQ ID NO: 2:
318      (i) SEQUENCE CHARACTERISTICS:
319           (A) LENGTH: 864 amino acids
320           (B) TYPE: amino acid
321           (D) TOPOLOGY: linear
323      (ii) MOLECULE TYPE: protein
325      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
327 Met Ala Ile Arg Arg Cys Trp Pro Arg Val Val Pro Gly Pro Ala Leu
328   1               5                  10                  15
330 Gly Trp Leu Leu Leu Leu Leu Asn Val Leu Ala Pro Gly Arg Ala Ser
331              20                  25                  30
333 Pro Arg Leu Leu Asp Phe Pro Ala Pro Val Cys Ala Gln Glu Gly Leu
334          35                  40                  45
336 Ser Cys Arg Val Lys Asn Ser Thr Cys Leu Asp Asp Ser Trp Ile His
337      50                  55                  60
339 Pro Lys Asn Leu Thr Pro Ser Ser Pro Lys Asn Ile Tyr Ile Asn Leu
340  65                  70                  75                  80
342 Ser Val Ser Ser Thr Gln His Gly Glu Leu Val Pro Val Leu His Val
343                  85                  90                  95
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/488,728

DATE: 05/16/2001
TIME: 16:07:04

Input Set : N:\Crf3\RULE60\09488728.txt
Output Set: N:\CRF3\05162001\I488728.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]